WHAT IS CLAIMED IS:

1. A method for analyzing gene expression data obtained from a plurality of microarrays having a plurality of probes, wherein the plurality of probes includes mismatch (MM) probe pairs having a mismatch value and perfect match (PM) probe pairs having a perfect match value, the method comprising the steps of:

obtaining image data corresponding to scanned microarrays, the image data for each scanned microarray comprising an image corresponding to the scanned probe intensities, scan date, and at least one chip identifier;

storing the image data for each scanned microarray in at least one database;

applying an automated quality control process, comprising the steps of

in a processor, processing the image data by applying at least a portion of a plurality of image processing metrics comprising algorithms adapted to identify one or more defects selected from the group consisting of haze, bright artifacts, dim artifacts, crop circles, snow, snow, misalignment, grid misalignment, high background intensity, saturation, scratches, cracks;

flagging any identified defects;

assigning a pass/fail status to each microarray based upon identified defects, if any;

storing the processed image data in the at least one database, the processed image data comprising the scanned probe intensities, the scan date, the at least one chip identifier, the pass/fail status, the applied image processing metrics, and the identified defects, if any ;

providing a user interface for searching the at least one database by selecting at least one chip parameter from the group consisting of scan date, the at least one chip identifier, the pass/fail status and the plurality of image processing metrics; and

displaying the results of the search.

2. The method of claim 1, wherein the step of processing the image data further comprises applying a mask to exclude data corresponding to defects.

3. The method of claim 1, wherein an image processing metric of the plurality comprises counting the MM probe pairs and PM probe pairs and flagging a

microarray as dim if the number of MM probe pairs is greater than the number of PM probe pairs.

4. The method of claim 1, wherein an image processing metric of the plurality comprises determining a normalized background variance by estimating a local background intensity and its spatial variation at a plurality of locations on the microarray corresponding to PM probes.

5. The method of claim 1, wherein an image processing metric of the plurality comprises:

estimating a local background intensity at a plurality of locations on the microarray corresponding to perfect match (PM) probe pairs;

dividing the microarray into inner and outer portions;

determining a mean background intensity for each of the inner and outer portions; and

using a ratio of mean background intensities of the outer and inner portions to flag crop circles.

6. The method of claim 1, wherein an image processing metric of the plurality comprises:

generating a model using the PM probe pairs from a set of microarrays;

applying the model to each microarray to be analyzed to determine a weights factor for each probe on the microarray.

7. The method of claim 1, wherein the defect is haze and the image processing metric is selected from the group consisting of vertical 10^{th} percentile peak to median ratio, maximum/minimum ratio for horizontal 25^{th} percentile profile, two edge ratios for horizontal 25^{th} percentile profile, two edge ratios for vertical 25^{th} percentile profile, maximum/minimum ratio for horizontal 75^{th} percentile profile, and two edge ratios for horizontal 75^{th} percentile profile.

8. The method of claim 1, wherein the defect is bright artifacts and the image processing metric is selected from the group consisting of oligo B2 mean intensity, spike-in offset, spike-in coefficient of determination, two edge ratios for horizontal 25^{th} percentile profile, two edge ratios for vertical 25^{th} percentile profile, two edge ratios for horizontal 75^{th} percentile profile, probe pair difference outlier horizontal variance, vertical probe pair difference outlier, negative probe pair

horizontal and vertical variance, negative probe pair horizontal and vertical maximum/minimum ratio, local background normalized variance.

9. The method of claim 1, wherein an image processing metric of the plurality comprises a ratio of the natural log of a mean intensity of non-control oligonucleotides to the natural log of an image fifth percentile.

10. An automated system for analyzing gene expression data obtained from a plurality of chips having a plurality of probes, wherein the plurality of probes includes mismatch (MM) probe pairs having a mismatch value and perfect match (PM) probe pairs having a perfect match value, the system comprising:

a database for storing image data for a plurality of scanned chips comprising an image corresponding to scanned probe intensities and a plurality of chip parameters corresponding to the scanned chip, wherein the chip parameters are selected from a group consisting of scan date, chip type, lot number, image processing metrics, and pass/fail status;

a user interface for receiving a user query comprising at least one chip parameter and for displaying information responsive to the query;

a processor for processing the image data for quality control by applying at least one of a plurality of image processing metrics adapted to identify defects selected from the group consisting of haze, bright artifacts, dim artifacts, crop circles, snow, snow, misalignment, grid misalignment, high background intensity, saturation, scratches, cracks, and for searching the database for records corresponding to the selected at least one chip parameter.

11. The system of claim 10, wherein the processor is further operable to apply a mask to exclude data corresponding to defects.

12. The system of claim 10, wherein an image processing metric of the plurality comprises counting the MM probe pairs and PM probe pairs and flagging a microarray as dim if the number of MM probe pairs is greater than the number of PM probe pairs.

13. The system of claim 10, wherein an image processing metric of the plurality comprises determining a normalized background variance by estimating a local background intensity and its spatial variation at a plurality of locations on the microarray corresponding to PM probes.

14. The system of claim 10, wherein an image processing metric of the plurality comprises:

estimating a local background intensity at a plurality of locations on the microarray corresponding to perfect match (PM) probe pairs;

dividing the microarray into inner and outer portions;

determining a mean background intensity for each of the inner and outer portions; and

using a ratio of mean background intensities of the outer and inner portions to flag crop circles.

15. The system of claim 10, wherein an image processing metric of the plurality comprises:

generating a model using the PM probe pairs from a set of microarrays;

applying the model to each microarray to be analyzed to determine a weights factor for each probe on the microarray.

16. The system of claim 10, wherein the defect is haze and the image processing metric is selected from the group consisting of vertical 10^{th} percentile peak to median ratio, maximum/minimum ratio for horizontal 25^{th} percentile profile, two edge ratios for horizontal 25^{th} percentile profile, two edge ratios for vertical 25^{th} percentile profile, maximum/minimum ratio for horizontal 75^{th} percentile profile, and two edge ratios for horizontal 75^{th} percentile profile.

17. The system of claim 10, wherein the defect is bright artifacts and the image processing metric is selected from the group consisting of oligo B2 mean intensity, spike-in offset, spike-in coefficient of determination, two edge ratios for horizontal 25^{th} percentile profile, two edge ratios for vertical 25^{th} percentile profile, two edge ratios for horizontal 75^{th} percentile profile, probe pair difference outlier horizontal variance, vertical probe pair difference outlier, negative probe pair horizontal and vertical variance, negative probe pair horizontal and vertical maximum/minimum ratio, local background normalized variance.

18. The system of claim 10, wherein an image processing metric of the plurality comprises a ratio of the natural log of a mean intensity of non-control oligonucleotides to the natural log of an image fifth percentile.

19. A method for determining quality of a microarray comprising a plurality of probes including PM probes, the method comprising:

in a set of microarrays comprising a plurality of transcripts, determining a probe weight for each PM probe using RMA analysis; and

calculating a relative weight factor for each transcript by taking the inverse of the square root of the sum of the probe weights for each PM probe;

wherein a higher relative weight factor value corresponds to a lower quality microarray.

20. The method of claim 19, wherein RMA analysis comprises:

background correcting a PM probe value for each PM probe;

$\log_2$ transforming the background-corrected PM probe values;

quantile normalizing the $\log_2$ transformed probe values for the set of microarrays; and

applying median polish to the quantile normalized values to obtain the probe weight for each PM probe.

21. A method for determining quality of a microarray comprising a plurality of probes including PM probes, the method comprising:

in a set of microarrays comprising a plurality of transcripts, determining a probe weight for each PM probe using RMA analysis; and

calculating a quality metric according to the relationship:

$$\overline{w} = \frac{1}{\sqrt{\sum_{j=1}^{J} w_j}}$$, where w_j is the weight of the j^{th} PM probe.

22. The method of claim 21, wherein RMA analysis comprises:

background correcting a PM probe value for each PM probe;

$\log_2$ transforming the background-corrected PM probe values;

quantile normalizing the $\log_2$ transformed probe values for the set of microarrays; and

applying median polish to the quantile normalized values to obtain the probe weight for each PM probe.

23. A method for determining quality of a microarray comprising a plurality of probes including PM probes, the method comprising:

in a set of microarrays comprising a plurality of transcripts, determining a probe weight for each PM probe using RMA analysis; and

calculating a quality metric according to the relationship:

$\sum_j \sum_k w_{jk}^{-x}, \forall j,k$,where w_{jk} is the weight of the j^{th} PM probe of transcript k, and $x = 1$ or 2.

24. The method of claim 23, wherein RMA analysis comprises:

background correcting a PM probe value for each PM probe;

$\log_2$ transforming the background-corrected PM probe values;

quantile normalizing the $\log_2$ transformed probe values for the set of microarrays; and

applying median polish to the quantile normalized values to obtain the probe weight for each PM probe.

25. A method for determining quality of a microarray comprising a plurality of probes including PM probes, the method comprising:

in a set of microarrays comprising a plurality of transcripts, determining a probe weight for each PM probe using RMA analysis; and

calculating a quality metric according to the relationship:

$\sum_j \sum_k (1 - w_{jk}), \forall j,k$, where w_{jk} is the weight of the j^{th} PM probe of transcript k.

26. The method of claim 25, wherein RMA analysis comprises:

background correcting a PM probe value for each PM probe;

$\log_2$ transforming the background-corrected PM probe values;

quantile normalizing the $\log_2$ transformed probe values for the set of microarrays; and

applying median polish to the quantile normalized values to obtain the probe weight for each PM probe.